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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=1; day=6; hr=14; min=22; sec=50; ms=92; ]

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Application No: 10522106 Version No: 3.0

Input Set:

Output Set:

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Started:      2009-12-15 16:22:28.242
Finished:    2009-12-15 16:22:35.214
Elapsed:     0 hr(s) 0 min(s) 6 sec(s) 972 ms
Total Warnings: 14
Total Errors:  66
No. of SeqIDs Defined: 36
Actual SeqID Count: 36

```

[illegible]

**Input Set:**

**Output Set:**

**Started:** 2009-12-15 16:22:28.242  
**Finished:** 2009-12-15 16:22:35.214  
**Elapsed:** 0 hr(s) 0 min(s) 6 sec(s) 972 ms  
**Total Warnings:** 14  
**Total Errors:** 66  
**No. of SeqIDs Defined:** 36  
**Actual SeqID Count:** 36

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (17)
E 300	Invalid codon found Thr SEQID (17) POS: 1153
E 300	Invalid codon found Ala SEQID (17) POS: 1156
E 300	Invalid codon found Val SEQID (17) POS: 1159
E 300	Invalid codon found His SEQID (17) POS: 1162
E 300	Invalid codon found Thr SEQID (17) POS: 1165
E 300	Invalid codon found Leu SEQID (17) POS: 1168
E 300	Invalid codon found Ala SEQID (17) POS: 1171
E 300	Invalid codon found His SEQID (17) POS: 1174
E 300	Invalid codon found Val SEQID (17) POS: 1177
E 300	Invalid codon found Thr SEQID (17) POS: 1180
E 300	Invalid codon found Cys SEQID (17) POS: 1183
E 300	Invalid codon found Asp SEQID (17) POS: 1186
E 300	Invalid codon found Phe SEQID (17) POS: 1189
E 300	Invalid codon found Pro SEQID (17) POS: 1192
E 300	Invalid codon found Arg SEQID (17) POS: 1195
E 300	Invalid codon found Leu SEQID (17) POS: 1198
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)

**Input Set:**

**Output Set:**

**Started:** 2009-12-15 16:22:28.242  
**Finished:** 2009-12-15 16:22:35.214  
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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
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W 213	Artificial or Unknown found in <213> in SEQ ID (29)
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W 213	Artificial or Unknown found in <213> in SEQ ID (32)
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W 213	Artificial or Unknown found in <213> in SEQ ID (34)
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# SEQUENCE LISTING

<110> Kogel, Karl-Heinz  
Huckelhoven, Ralph  
Trujillo, Marco

<120> Method for Obtaining a Pathogen Resistance in Plants

<130> 12810-00067-US

<140> 10522106

<141> 2009-12-15

<150> PCT/EP03/07589

<151> 2003-07-14

<150> DE 10233327.0

<151> 2002-07-22

<160> 36

<170> PatentIn Ver. 3.3

<210> 1

<211> 337

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (2)..(337)

<223> coding for NADPH oxidase (fragment)

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1

5

10

15

att gag atg cac aac tat ctc aca agt gtt tat gag gaa ggg gat gct 97

Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala

20

25

30

cgg tca gca ctc atc aca atg ctg caa gct ctc aac cat gcc aag aat 145

Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn

35

40

45

ggg gtc gat gta gtg tct ggm act cga gtc cgg aca cat ttt gca aga 193

Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg

50

55

60

cca aat ttt aag agg gtg ctg tct aag gta gcc gcc aaa cat cct tat 241

Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr

65

70

75

80

gcc aag ata gga gtg ttc tat tgc gga gct cca gtt ctg gcg cag gaa 289

Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu

85

90

95

cta agc aac ctt tgc cat gag ttc aat ggc aaa tgc acg aca aaa ttc 337

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100

105

110

<210> 2

<211> 112

<212> PRT  
<213> Hordeum vulgare

<220>  
<221> misc\_feature  
<222> (55)..(55)  
<223> The 'Xaa' at location 55 stands for Gly.

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Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala  
20 25 30  
Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn  
35 40 45  
Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg  
50 55 60  
Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr  
65 70 75 80  
Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu  
85 90 95  
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100 105 110

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<212> DNA  
<213> Oryza sativa

<220>  
<221> CDS  
<222> (1)..(2829)  
<223> coding for NADPH oxidase

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acg aca ccg cgg tcg ctg agc acg ggc tcg tcg ccg cgc ggg tcc gac 96  
Thr Thr Pro Arg Ser Leu Ser Thr Gly Ser Ser Pro Arg Gly Ser Asp  
20 25 30  
gac cgg agc tcc gac gac ggg gag gag ctg gtc gag gtc acg ctc gac 144  
Asp Arg Ser Ser Asp Asp Gly Glu Glu Leu Val Glu Val Thr Leu Asp  
35 40 45  
ctg cag gac gac gac acc att gtg ctt cgg agc gtc gag ccc gcg gcg 192  
Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala Ala  
50 55 60  
gcg gcg gcg gcg ggg gtg ggg gcg ggg gcg ggg gcg gcg tcg gcg cgg 240  
Ala Ala Ala Ala Gly Val Gly Ala Gly Ala Gly Ala Ala Ser Ala Arg  
65 70 75 80  
ggg gag ctc acg ggt ggc ccg tcg tcg tcg tcg tcg cgg tcg agg tcg 288  
Gly Glu Leu Thr Gly Gly Pro Ser Ser Ser Ser Ser Arg Ser Arg Ser  
85 90 95  
ccg tcg atc cgg agg agc tcg tcg cac cgg ctg ctg cag ttc tcg cag 336  
Pro Ser Ile Arg Arg Ser Ser Ser His Arg Leu Leu Gln Phe Ser Gln  
100 105 110  
gag ctc aag gcg gag gcc atg gcc cgg gcg cgg cag ttc tcg cag gac 384

Glu	Leu	Lys	Ala	Glu	Ala	Met	Ala	Arg	Ala	Arg	Gln	Phe	Ser	Gln	Asp	
		115					120					125				
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Leu	Thr	Lys	Arg	Phe	Gly	Arg	Ser	His	Ser	Arg	Ser	Glu	Ala	Gln	Ala	
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ccg	tcg	ggc	ctc	gag	tcc	gcg	ctc	gcc	gcc	cgc	gcc	gcg	cgg	cgg	cag	480
Pro	Ser	Gly	Leu	Glu	Ser	Ala	Leu	Ala	Ala	Arg	Ala	Ala	Arg	Arg	Gln	
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cgc	gcg	cag	ctc	gac	cgc	aca	cgc	tcc	ggc	gcc	cac	aag	gcg	ctc	cgc	528
Arg	Ala	Gln	Leu	Asp	Arg	Thr	Arg	Ser	Gly	Ala	His	Lys	Ala	Leu	Arg	
				165					170					175		
ggc	ctc	cgc	ttc	atc	agc	agc	aac	aag	gcc	aac	aac	gcc	tgg	atg	gag	576
Gly	Leu	Arg	Phe	Ile	Ser	Ser	Asn	Lys	Ala	Asn	Asn	Ala	Trp	Met	Glu	
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Val	Gln	Ala	Asn	Phe	Asp	Arg	Leu	Ala	Arg	Asp	Gly	Tyr	Leu	Ser	Arg	
		195					200				205					
tcc	gac	ttc	gcc	gaa	tgc	atc	ggg	atg	acg	gaa	tcg	aag	gag	ttc	gcg	672
Ser	Asp	Phe	Ala	Glu	Cys	Ile	Gly	Met	Thr	Glu	Ser	Lys	Glu	Phe	Ala	
		210				215				220						
ctc	gag	ctg	ttc	gac	acg	ctg	agc	cgg	cga	cga	cag	atg	aag	gtg	gac	720
Leu	Glu	Leu	Phe	Asp	Thr	Leu	Ser	Arg	Arg	Arg	Gln	Met	Lys	Val	Asp	
		225				230				235				240		
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Thr	Ile	Asn	Lys	Asp	Glu	Leu	Arg	Glu	Ile	Trp	Gln	Gln	Ile	Thr	Asp	
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aac	agc	ttc	gac	tcc	cgt	ctc	caa	atc	ttc	ttc	gaa	atg	gtg	gat	aag	816
Asn	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Ile	Phe	Phe	Glu	Met	Val	Asp	Lys	
		260						265					270			
aac	gcg	gac	ggc	cgg	att	acg	gag	gcg	gag	gtg	aaa	gag	att	att	atg	864
Asn	Ala	Asp	Gly	Arg	Ile	Thr	Glu	Ala	Glu	Val	Lys	Glu	Ile	Ile	Met	
		275					280					285				
ttg	agc	gcg	tct	gcc	aat	aaa	ctg	tcg	agg	ctt	aag	gag	caa	gca	gaa	912
Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	Gln	Ala	Glu	
		290				295				300						
gag	tac	gcc	gct	ttg	atc	atg	gag	gag	ctt	gat	cct	gaa	ggg	ctc	ggc	960
Glu	Tyr	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Glu	Gly	Leu	Gly	
		305				310				315				320		
tac	att	gag	cta	tgg	caa	ttg	gag	aca	ctt	ctg	ttg	cag	aaa	gat	acc	1008
Tyr	Ile	Glu	Leu	Trp	Gln	Leu	Glu	Thr	Leu	Leu	Leu	Gln	Lys	Asp	Thr	
				325					330					335		
tat	atg	aac	tat	agt	cag	gcc	ctt	agt	tac	aca	agc	caa	gca	ctg	agc	1056
Tyr	Met	Asn	Tyr	Ser	Gln	Ala	Leu	Ser	Tyr	Thr	Ser	Gln	Ala	Leu	Ser	
				340					345					350		
cag	aat	ctt	gca	ggg	cta	agg	aag	aag	agt	tca	atc	cgc	aaa	ata	agc	1104
Gln	Asn	Leu	Ala	Gly	Leu	Arg	Lys	Lys	Ser	Ser	Ile	Arg	Lys	Ile	Ser	
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acc	tct	tta	agc	tac	tat	ttc	gag	gac	aac	tgg	aaa	cgt	tta	tgg	gtg	1152
Thr	Ser	Leu	Ser	Tyr	Tyr	Phe	Glu	Asp	Asn	Trp	Lys	Arg	Leu	Trp	Val	
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Leu	Ala	Leu	Trp	Ile	Gly	Ile	Met	Ala	Gly	Leu	Phe	Thr	Trp	Lys	Phe	
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Met	Gln	Tyr	Arg	Asn	Arg	Tyr	Val	Phe	Asp	Val	Met	Gly	Tyr	Cys	Val	
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Thr	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Leu	Asn	Met	Ala	Ile	
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atc	ctc	ctg	cca	gta	tgc	cgt	aac	acc	att	act	tgg	ttg	cga	agt	aca	1344
Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Ser	Thr	
			435				440					445				
agg	gct	gca	cgg	gca	cta	cct	ttt	gat	gac	aac	atc	aac	ttc	cac	aag	1392
Arg	Ala	Ala	Arg	Ala	Leu	Pro	Phe	Asp	Asp	Asn	Ile	Asn	Phe	His	Lys	
			450				455				460					
act	att	gca	gca	gca	att	gtg	ggt	ggt	ata	atc	ctc	cat	gca	ggg	aac	1440
Thr	Ile	Ala	Ala	Ala	Ile	Val	Val	Gly	Ile	Ile	Leu	His	Ala	Gly	Asn	
						470				475					480	
cac	ctt	gta	tgc	gat	ttt	cca	cgg	tta	ata	aaa	tca	tca	gat	gag	aag	1488
His	Leu	Val	Cys	Asp	Phe	Pro	Arg	Leu	Ile	Lys	Ser	Ser	Asp	Glu	Lys	
					485				490					495		
tat	gct	cct	ttg	ggc	cag	tat	ttt	ggg	gaa	ata	aag	cca	aca	tat	ttt	1536
Tyr	Ala	Pro	Leu	Gly	Gln	Tyr	Phe	Gly	Glu	Ile	Lys	Pro	Thr	Tyr	Phe	
			500					505					510			
aca	ttg	gtc	aaa	gga	gtg	gag	ggc	atc	act	ggg	gta	atc	atg	gtt	gta	1584
Thr	Leu	Val	Lys	Gly	Val	Glu	Gly	Ile	Thr	Gly	Val	Ile	Met	Val	Val	
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tgc	atg	ata	att	gct	ttt	act	cta	gca	acc	cgg	tgg	ttc	cgc	cgt	agc	1632
Cys	Met	Ile	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe	Arg	Arg	Ser	
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Leu	Val	Lys	Leu	Pro	Arg	Pro	Phe	Asp	Lys	Leu	Thr	Gly	Phe	Asn	Ala	
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Phe	Trp	Tyr	Ser	His	His	Leu	Phe	Ile	Ile	Val	Tyr	Ile	Ala	Leu	Ile	
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gtt	cat	gga	gag	tgt	cta	tac	ctt	att	cat	gtc	tgg	tac	aga	aga	acg	1776
Val	His	Gly	Glu	Cys	Leu	Tyr	Leu	Ile	His	Val	Trp	Tyr	Arg	Arg	Thr	
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Pro	Thr	Phe	Arg	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Phe	Val	Gln	Cys	Pro	
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Gly	Asp	Asp	Tyr	Leu	Ser	Ile	His	Val	Arg	Gln	Leu	Gly	Asp	Trp	Thr	
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Arg	Glu	Leu	Lys	Arg	Val	Phe	Ala	Ala	Ala	Cys	Glu	Pro	Pro	Ala	Gly	
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Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Asn	Asn	Ile	Ile	Lys	Met		
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Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Val	Met	Asn	Glu	Ile		
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gct	gac	ttg	gat	caa	agg	aat	atc	att	gag	atg	cac	aac	tac	cta	aca	2544	
Ala	Asp	Leu	Asp	Gln	Arg	Asn	Ile	Ile	Glu	Met	His	Asn	Tyr	Leu	Thr		
			835				840				845						
agc	gtc	tat	gag	gag	ggg	gat	gcc	agg	tca	gca	ctc	atc	acc	atg	ctc	2592	
Ser	Val	Tyr	Glu	Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu	Ile	Thr	Met	Leu		
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caa	gct	ctg	aac	cat	gcc	aag	aat	gga	gtt	gat	att	gtc	tct	ggg	aca	2640	
Gln	Ala	Leu	Asn	His	Ala	Lys	Asn	Gly	Val	Asp	Ile	Val	Ser	Gly	Thr		
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aaa	gtc	cgg	aca	cat	ttt	gca	cga	cca	aat	tgg	aga	aag	gtc	ctt	tct	2688	
Lys	Val	Arg	Thr	His	Phe	Ala	Arg	Pro	Asn	Trp	Arg	Lys	Val	Leu	Ser		
			885					890				895					
aaa	att	tcc	tcc	aag	cat	cca	tat	gcc	aaa	ata	ggg	gta	ttc	tac	tgt	2736	
Lys	Ile	Ser	Ser	Lys	His	Pro	Tyr	Ala	Lys	Ile	Gly	Val	Phe	Tyr	Cys		
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			915				920				925						
aac	ggg	aaa	tgc	aca	acg	aag	ttc	gaa	ttc	cat	aag	gag	cat	ttc	tga	2832	
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<210> 4

<211> 943

<212> PRT

<213> Oryza sativa

<400> 4

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			20					25					30				
Asp	Arg	Ser	Ser	Asp	Asp	Gly	Glu	Glu	Leu	Val	Glu	Val	Thr	Leu	Asp		
			35				40					45					
Leu	Gln	Asp	Asp	Asp	Thr	Ile	Val	Leu	Arg	Ser	Val	Glu	Pro	Ala	Ala		
			50				55				60						

Ala	Ala	Ala	Ala	Gly	Val	Gly	Ala	Gly	Ala	Gly	Ala	Ala	Ser	Ala	Arg	65	70	75	80
Gly	Glu	Leu	Thr	Gly	Gly	Pro	Ser	Ser	Ser	Ser	Ser	Arg	Ser	Arg	Ser	85	90	95	
Pro	Ser	Ile	Arg	Arg	Ser	Ser	Ser	His	Arg	Leu	Leu	Gln	Phe	Ser	Gln	100	105	110	
Glu	Leu	Lys	Ala	Glu	Ala	Met	Ala	Arg	Ala	Arg	Gln	Phe	Ser	Gln	Asp	115	120	125	
Leu	Thr	Lys	Arg	Phe	Gly	Arg	Ser	His	Ser	Arg	Ser	Glu	Ala	Gln	Ala	130	135	140	
Pro	Ser	Gly	Leu	Glu	Ser	Ala	Leu	Ala	Ala	Arg	Ala	Ala	Arg	Arg	Gln	145	150	155	160
Arg	Ala	Gln	Leu	Asp	Arg	Thr	Arg	Ser	Gly	Ala	His	Lys	Ala	Leu	Arg	165	170	175	
Gly	Leu	Arg	Phe	Ile	Ser	Ser	Asn	Lys	Ala	Asn	Asn	Ala	Trp	Met	Glu	180	185	190	
Val	Gln	Ala	Asn	Phe	Asp	Arg	Leu	Ala	Arg	Asp	Gly	Tyr	Leu	Ser	Arg	195	200	205	
Ser	Asp	Phe	Ala	Glu	Cys	Ile	Gly	Met	Thr	Glu	Ser	Lys	Glu	Phe	Ala	210	215	220	
Leu	Glu	Leu	Phe	Asp	Thr	Leu	Ser	Arg	Arg	Arg	Gln	Met	Lys	Val	Asp	225	230	235	240
Thr	Ile	Asn	Lys	Asp	Glu	Leu	Arg	Glu	Ile	Trp	Gln	Gln	Ile	Thr	Asp	245	250	255	
Asn	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Ile	Phe	Phe	Glu	Met	Val	Asp	Lys	260	265	270	
Asn	Ala	Asp	Gly	Arg	Ile	Thr	Glu	Ala	Glu	Val	Lys	Glu	Ile	Ile	Met	275	280	285	
Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	Gln	Ala	Glu	290			